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Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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 SPTREMBL_15:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungl:*
4: sp_human:*
5: sp_mammal:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
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12: sp_vertebrate:
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14: sp_unclassifie
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245
1 SQRQFQECQHCHQQEQRPE.....QCVRECREKYQENPWRGER 42
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Gapop 10.0 , Gapext 0.5
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sp_plant:*
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16.424 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6/.5	89	68	69	69.5	69.5	70	70	72	72	72.5	74	74	91	94	98	99	103	111.5	Score		
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ALIGNMENTS

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2 OROFQECOOHCHQQEQRPEKKQQCVRECREKYQENPWRGE 41 : : : :: : :	Query Match Best Local Similarity 50.0%; Pred. No. 6.8e-06; Matches 20; Conservative 9; Mismatches 10; Indels 1; Gaps 1;	AA;	L 1 24	PD081059; -; 1.	PFAM; PF00546; Seedstore_7s; 1.	MENDEL; 30919; Thecc;1188;30919.	HSSP; P02853; 2PHL.	X62626; CAA44494.1;		Plant Mol. Biol. 18:1173-1176(1992).	are and nu		MEDLINE=92288309; PubMed=1600151;	TISSUE=LEAVES;	SEQUENCE FROM N.A.	(2) - : ::::	NCBI_TaxID=3641;		ca; itacheophyta; spermatophy	STATEMENT OF THE CONTROL OF THE CONT	Thoopers are Arrest	VICILIN PRECURSOR.	(TrEMBLrel. 15, Last	(TrEMBLrel. 01,	01-NOV-1996 (TrEMBLrel. 01, Created)		043358 PRELIMINARY: PRT: 525 AA.	ILT 1

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R EMBL; AF161885; AAD54246.1; -.

R INTERPRO; IPRON'''
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Best Local :
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; APO66055; AAF18269.1; -.
HSSP; P02853; 2PHL.
INTERPRO; IPRO01113; -.
                                                                                                                                                                                                                                                         Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
                                                                                                                                                                                                                                                                                                AMP2
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STRAIN-CV. SUNLAND: TISSUE-SOMATIC EMBRYO LINE;
Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;
"Identification and cloning of a cDNA encoding a vicilin-like protein,"
"Identification and cloning of a cDNA encoding a vicilin-like protein,"
"Identification and cloning of a cDNA encoding a vicilin-like protein,"
"Identification and cloning of a cDNA encoding a vicilin-like protein,"
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Juglans regia (English walnut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sj
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Fagales; Juglandaceae; Juglans.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                    VICILIN PRECURSOR
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01-MAY-2000
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  QRQFQECQQHCHQQEQRPEKKQQCVRECREKYQE-----NPWRG
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O9SPL5;

O1-MAY-2000 (TrEMBLrel. 1

O1-MAY-2000 (TrEMBLrel. 1

O1-OCT-2000 (TrEMBLrel. 1
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Marcus J.P., Goulter K.C., Green J.L., Manner:
"A family of antimicrobial peptides is product
globulin protein in Macadamia Integrifolia.";
Plant J. 0:0-0(1999).

EMBL; AF161884; AAD54245.1; -.
HSSP; P02853; 2PHL.
INTERPRO; IPR0011113; -.
                                                                                                TISSUE-NUT KERNEL;
Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
"A family of antimicrobial peptides is produced by p.
globulin protein in Macadamia integrifolia kernels."
plant J. 0:0-0(1999).
EMBL; AF161883; AAD54244.1; -.
HSSP; P02853; 2PHL.
INTERPRO; IPRO01113; -.
                                                                                                                                                                                                              AMP2.

Macadamia integrifolia (Macadamia nut).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;

Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
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Q9SPL4;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-CT-2000 (TrEMBLrel. 15,
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
NCBI_TaxID=60698;
                                                                            PFAM; PF00546; Seedstore_7s; SEQUENCE 666 AA; 78217 MW
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SEQUENCE 666 AA; 78243 MW;
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basun A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heimann T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibsgwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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01-MAY-2000
01-MAY-2000
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Eukaryota; Viridiplantae; I
Magnoliophyta; Liliopsida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
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Pterygota;
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17; Conserv
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(TrEMBLrel. 10, Last sequence update)
(TremBLrel. 10, Last annotation update)
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36.2%;
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; Poales; Poaceae; Oryza.
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Last annotation update)
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Pred. No. 0.00
10; Mismatches
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Best Local S
Matches 13
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A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
Globs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
R EMBASE: FBgn0032497; CG6043.
R FINTERPRO; IPR002965; -.
R PRINTS; PR01217; PRICHEXTENSN.
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Best Local
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TILLIB S., Sedkov Y., Mizrokhi L.
Mech. Dev. 0:0-0(1995).
EMBL: 250038; CAA90349.1; -.
EMBL: 250038; CAA90349.1; -.
HSSP: P19793; 2NLL.
FLYBASE: FB990014844; Dvir\trx.
INTERPRO: IPRO01214; -.
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Q24742;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-OCT-2000 (TrEMBLrel. 1
 2995
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                                                                                                                                                        PFAM;
PFAM;
                                                                                                                                                                                      INTERPRO;
INTERPRO;
                                                                                                                                                                                                                                                                                                                                             Pterygota; Neoptera; Endopterygota; Dip
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                           PREDICTED TRITHORAX PROTEIN.
Drosophila virilis (Fruit fly).
Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                          PFAM; PF00856; SEQUENCE 382
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7244;
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                                                            Local Similarity 38.2 nes 13; Conservative
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                             2 QRQFQECQQHCHQQEQRPEKKQQCVRECREKYQE 35
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ООЕРОЕЕООНІНОООООООООООНМООНООООО 3028
                                                                                                                                                                       PF00628; PHD;
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                                                                                                                                          3828 AA;
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Q17401;
Q17401;
O1-JAN-1999
Q1-JAN-1999
Q1-JUN-2000
Q1-JUN-2000
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-!- SIMILARITY: BELONGS TO FAMILY UPF.
EMBL: 271177; CAA94867.1; -.
WORMPEP: AC3.3; CEO5133.
Hypothetical protein; Signal.
SIGNAL 1 21 POTENTIAL.
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01-JAN-1999 (TrEMBLrel. 09, La
01-JAN-1999 (TrEMBLrel. 09, La
HYPOTHETICAL 45.9 KDA PROTEIN
AC3.3.
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STRAIN-CV. TAINUNG 67;
TSENG M.J., Wang C.S., Hsu H.R.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
EMBL; U25969; AAD10370.1; -.
SEQUENCE 402 AA; 44252 MW; F03C86948F840060 CRC64;
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
EARLY EMBRYOGENESIS PROT
   HYPOTHETICAL AC3.4.
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STRAIN-BRISTOL N2;
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Rhabditidae; Pelode
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Eukaryota; Viridiplantae; Embryophyta;
Eugroliophyta; Liliopsida; Poales; Poac
NCBI_TaxID=4530;
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01-MAY-1999
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                                                                                                                                                                                                                                                                                                                                          OQCOQQCVQTQPIQQCQPQCQQQCVQQC
                                                                                                                                                                                                                                                                                                                                                                                                   QECQQHCHQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQCRKQCQHHHDQ--WKKQQCMQDCRQ-----WRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QECQQHC-HQQEQRPEKKQQCVRECREKYQENPWRGER 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 AA;
                            (TrEMBLrel. () (TrEMBLrel. () (TrEMBLrel. ) (TrEMBLrel. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                       -QEQRPEKKQQCVREC
                               KDA PROTEIN AC3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nematoda; Chromadorea; cinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.6%;
39.5%;
                                               09, Created)
09, Last sequence update)
14, Last annotation update)
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Last annotation update)
IN AC3.3 IN CHROMOSOME V
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 72; DB
Pred. No. 0.32
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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HYPOTHETICAL PROTEIN AC3.3.
; 951352A2AFF7E96C CRC64;
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                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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No. 0.
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                               IN CHROMOSOME
                                                                                                                                                                                        600
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1.32;
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                                                                                                                                                                                        A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Best Local S
Matches 15
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Best Local S
Matches 13
                                                                                   PROSITE; PS00867; CPSASE_2: UNKNOWN_1.
PRODOM; PD081059; -; 1.
Seed storage protein.
SEQUENCE 637 AA.
                                                                                                                                                                                                                                                                                                                       Q03678 PRELIMINARY;
Q03678;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-OCT-2000 (TrEMBLrel. 1
FETAL STORAGE PROTEIN.
                                                                                                                                                           chromosome mapping and regulation of Mol. Gen. Genet. 239:209-218(1993).
EMBL: M64372: AAA32936.1: -.
EMBL: M81719: AAA34269.1: -.
HSSP: P02853: 2PHL.
MENDEL: 8553: HOTVU:1188:8553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=93287988; PubMed=8510647;
                                                                                                                                                                                                                                                                                 Hordeum vulgare (Barley),
Eukaryota; Viridiplantae;
Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                BEG1 OR GBL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF01529; zf-DHHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcmurray A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                           "Barley embryo globulin 1 gene, Beg1: characterization chromosome mapping and regulation of expression.";
                                                                                                                                                                                                                                  Heck
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRODOM; PD003041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WORMPEP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO;
                                                                                                                                         NTERPRO; IPR000901;
                                        Local Similarity
nes 15; Conserv
 42
                                                                                                                                                                                                                                                                                                                                                                                                                           24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 46.4 es 13; Conservative
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                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                              6 QECQQHCHQ----QEQRPEKKQQCVREC
                                                                                                                                                                                                                                  G.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                          QQCVQRCRQERPR-YSHARCVQECRDDQQQHGRHEQEEEQGRGRGWHGE
                    QECQQHCHQQEQRPEKKQQCVRECREKYQEN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          003041; -; 1.

al protein; Transmembrane.
309 POTENTIA
447 467 POTENTIA
490 510 POTENTIA
6 287 GLN-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001594; -.
                                                                                                                                                                                                                                 Chamberlain A.C., Ho T.H.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600
                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.4%;
                                                28.6%;
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01,
15,
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                                                                                                                                                                                                                                                                                 and Triticum aestivum (Wheat) Embryophyta; Tracheophyta; Sp; Poales; Poaceae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 72; DB
Pred. No. 0.44
7; Mismatches
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POTENTIAL.
POTENTIAL.
GLN-RICH.
                                                Score 70;
Pred. No.
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504A5CE1BA72091B CRC64;
                                                                                         F323F4FF99947C3C CRC64;
                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           51
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                                                                                                                                                                                                                                                                                                                                                                          637
                                                   0
                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DВ
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                                                                                                                                                                                                                                                                                                                                   update)
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PROTEIN (PO
                                        13;
                    --- PWRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 600
                                                          Length 637;
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                           Spermatophyta;
89
                    41
                                                                                                                                                                                                                       of cDNA,
                                       14;
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                                       Gaps
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RESULT
Q9VE66
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Best Local
                             Q9VE66;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
CG14307 PROTEIN.
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O1-JAN-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
01-MAY-2000 (TrEMBLrel. 1
2C101.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                             Q9VE66
                                                                                                                                                                                                                                                                                                                           PFAM; PF00057; ldl_recept_a; 7.
PRINTS; PR00261; LDLRECEPTOR.
PROSITE; PS01209; LDLRA_1; 5.
PROSITE; PS50068; LDLRA_2; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
              Drosophila
                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                   Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-1997)
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                                                                                                                                        14
                                                                                                                                                                                                        4 QFQECQQHCHQQEQRPEKKQQCVRECREKYQEN 36
                                                                                                                                                                                                                                                                                                                                                                                               293395; CABO7705.1; -.
283112; CABO7705.1; JOINED.
283112; CABO5541.1; -.
293395; CABO5541.1; JOINED.
P01130; IAJJ.
                                                                                                                                                                                                                                  l Similarity 39.4
                                                                                                                                                                                                                                                                                                                                                                                  IPR002172; -
 melanogaster (Fruit )
Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                   905 AA;
                                                                                                             PRELIMINARY;
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                                                     Created)
Last sequence update)
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                                                                                                                                                                                                                               Score 70; DB
Pred. No. 1.1;
L1; Mismatches
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Last annotation update)
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               fly).
Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                   77DACE50D1A7BD24 CRC64;
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Drosophila melanogaster (Fruit fly)

13,

Last sequence update)
Last annotation updat

update)

CG12964

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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Meson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeb J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.M., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Spier E., Spradlence of Drosophila melanogaster.";
REITVASES: FRONCESCA. Gellan?
REITVASES: FRONCESCA. Gellan?
REITVASES: FRONCESCA. Gellan?
                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 15
                                                    09V7C5
09V7C5;
01-MAY-2000
01-MAY-2000
01-MAY-2000
                                U1-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
CG12964 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S. M., Subton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00096; zf-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLYBASE; FBgn0038624; CG14307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                    2 QROFQECQQHCHQQEQRPEKKQQCVRECREKY---QENPWR
                                                                                                                                                                                                                                QQQQQQQQHQHQQQQQHQQSQQQQQQQQQQQHQYLGWNYGAWR 155
                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                             Similarity 36.
                                                                                                                                                                                                                                                                                                                                                                                                       '00096; zf-C2H2; 1.
PS00028; ZINC_FINGER_C2H2;
328 AA; 38204 MW; 4C16
                                                                                            (TrEMBLrel. 13,
                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               28.4%;
                                                                                                                                                                                                                                                                                                             10;
                                                                                            Created)
                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           4C169889ABFD0899 CRC64;
                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                    925
                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                 51;
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                                                                                                                                                                                                                                                                                                             13:
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                                                                                                                                                                                                                                                                                                             Indels
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В
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                                                                                                            Query Match
Best Local :
                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
439 QQQHQYQQQHQHQHQAPQQHQQQAPQ-QQQYQKPP 473
                                          2 QRQFQECQQHCHQQEQRPEKKQQCVRECREKYQENP 37
                                                                                   l Similarity
15; Conserv
                                                                                     Conservative
                                                                                                          28.4%;
41.7%;
                                                                                     8; Mismatches
                                                                                                          Score 69.5;
Pred. No. 1.
                                                                                                                              DB 5; Length 925;
                                                                                   12;
                                                                                   Indels
                                                                                   1;
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Search completed: March 1, Job time: 1580 sec

2001, 16:09:36